FIGURE 1

A

Nucleotide

ATGAAGAGCGTCTTGCTGCTGACCACGCTCCTCGTGCCTGCACACCTGGTGGCCGCCTGGAGCAA
TAATTATGCGGTGGACTGCCCTCAACACTGTGACAGCAGTGAGTGCAAAAGCAGCCCGCGCTGCA
AGAGGACAGTGCTCGACGACTGTGGCTGCTGCCGAGTGTGCGCTGCAGGGCGGGGAGAAACTTGC
TACCGCACAGTCTCAGGCATGGATGGCATGAAGTGTGGCCCGGGGCTGAGGTGTCAGCCTTCTAA
TGGGGAGGATCCTTTTGGTGAAGAGTTTGGTATCTGCAAAGACTGTCCCTACGGCACCTTCGGGA
TGGATTGCAGAGAGACCTGCAACTGCCAGTCAGGCATCTGTGACAGGGGGACGGGAAAATGCCTG
AAATTCCCCTTCTTCCAATATTCAGTAACCAAGTCTTCCAACAGATTTGTTTCTCTCACGGAGCA
TGACATGGCATCTGGAGATGGCAATATTGTGAGAGAAGAAGTTGTGAAAGAGAATGCTGCCGGGT
CTCCCGTAATGAGGAAATGGTTAAATCCACGCTGA SEQ ID NO:1

Protein

MKSVLLLTTLLVPAHLVAAWSNNYAVDCPQHCDSSECKSSPRCKRTVLDDCGCCRVCAAGRGETC
YRTVSGMDGMKCGPGLRCQPSNGEDPFGEEFGICKDCPYGTFGMDCRETCNCQSGICDRGTGKCL
KFPFFQYSVTKSSNRFVSLTEHDMASGDGNIVREEVVKENAAGSPVMRKWLNPR

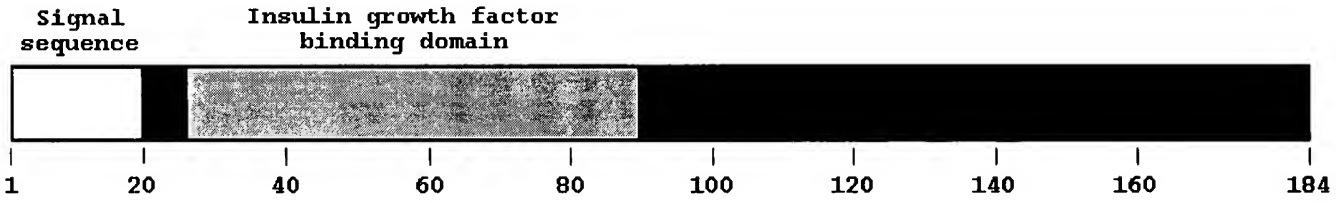
SEQ ID NO:2

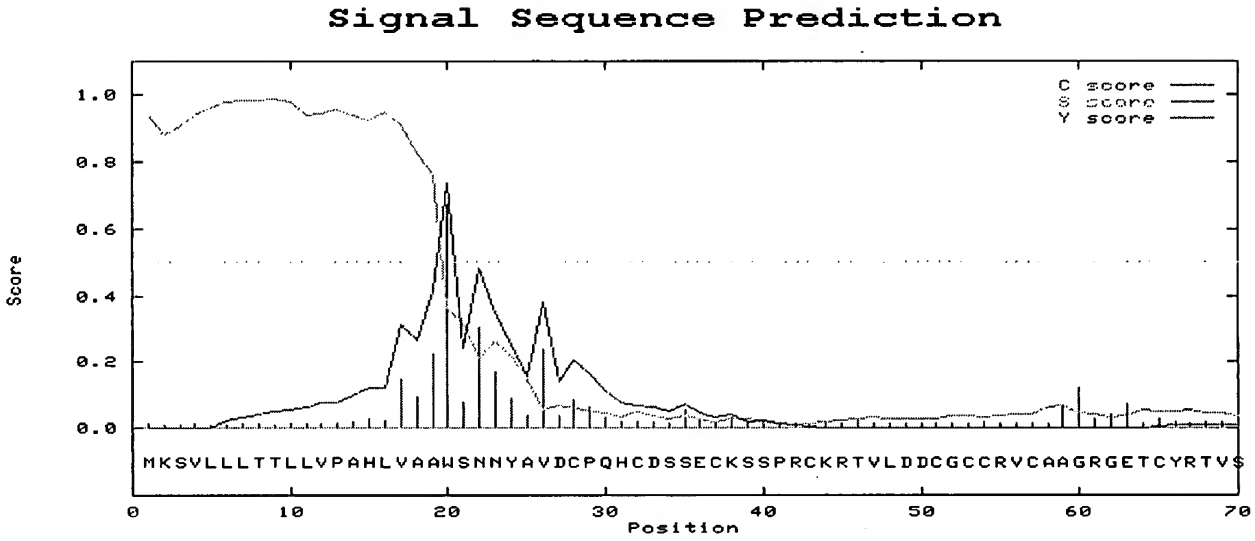
B

Insulin Growth Factor Binding Domain Homology

```
ESM-1  26 VDCPQHCDSSECKSSPR--CKRTVLDDCGCCRVCAAGRGETCYRTVSGMDGMKCGPGLRCQPSNGED 90 SEQ ID NO:3
IGFBD   1 ARCP-PCSPARCPPEPPGCAELVVLDGCGCCPVCARQEGEPC-----GVYTPPCAPGLRCDPPPGEE 61 SEQ ID NO:4
```

FIGURE 2





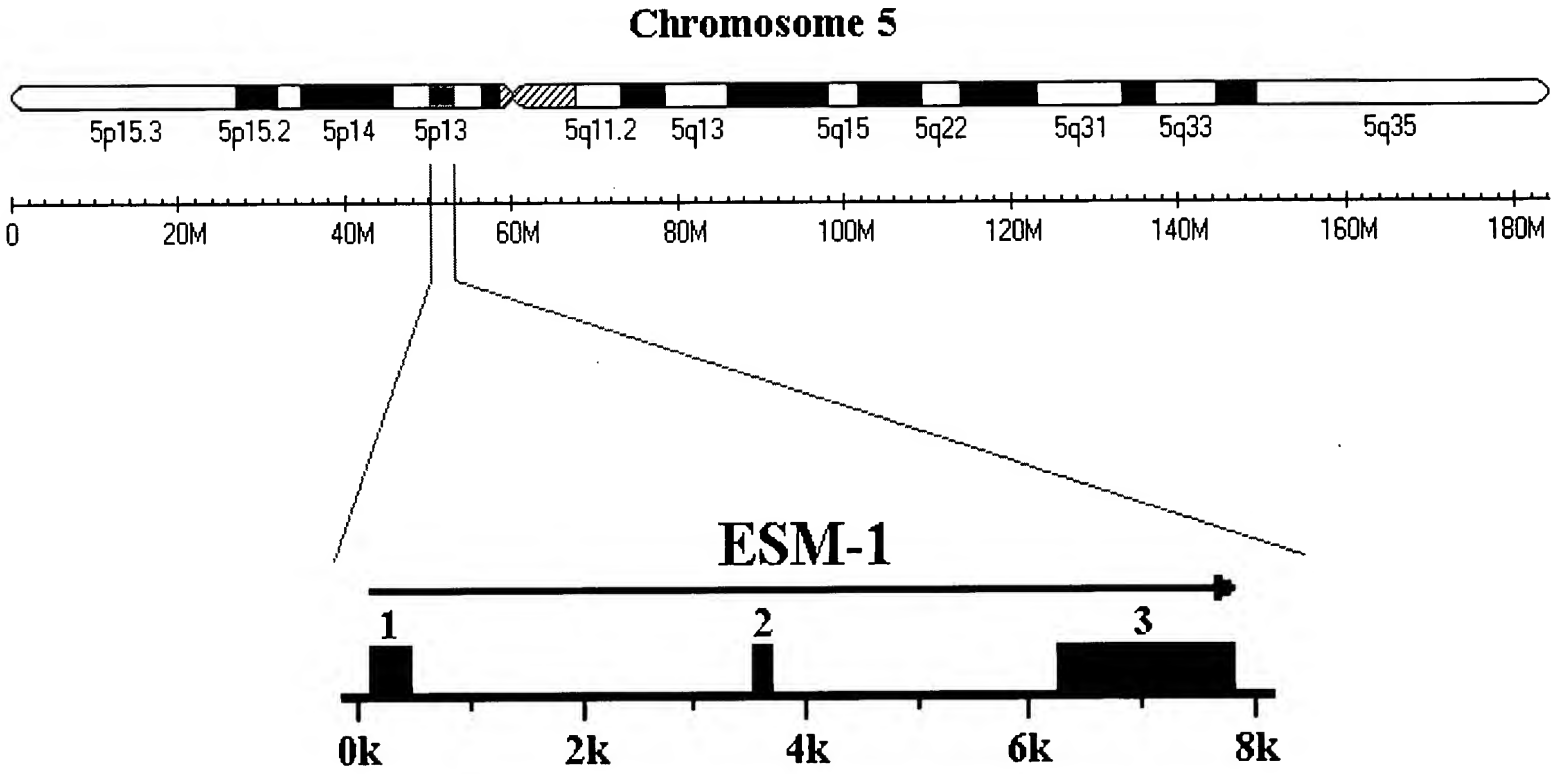
# Measure	Position	Value	Cutoff	signal peptide?
max. C	20	0.673	0.33	YES
max. Y	20	0.737	0.32	YES
max. S	9	0.990	0.82	YES
mean S	1-19	0.932	0.47	YES

Most likely cleavage site between pos. 19 and 20: VAA-WS

FIGURE 3


Rat_ESM1 MKSLLLLTTLLIPLHLGMAWSAKYAVDCPEHCDNTECRSSLRCKRTVLDDCGCCQVCAAGPGETCYRTVSGMDGV 75
Mouse_ESM1 MKSLLLLTTLLVPLHLGMAWSAKYAVDCPEHCDKTECRSSLRCKRTVLDDCGCCQVCAAGPGETCYRTVSGMDGV 75
Human_ESM1 MKSQLLLTTLLVPAHLVAAWSNNYAVDCPQHCDSSECKSSPRCKRTVLDDCGCCRVCAAGRGETCYRTVSGMDGQ 75
Rat_ESM1 KCGPGLKCHFYSEEDDFGDEFGQCKDCPYGTFGMDCKETCNCQSGICDRVTGRCLDFPFFQYAAAKSPSRTSASQ 150
Mouse_ESM1 KCGPGLKCHFYSEEDDFGDEFGICKDCPYGTFGMECKETCNCQSGICDRVTGRCLDFPFFQYAAAKSPSRTSASH 150
Human_ESM1 KCGPGLRCQPSNGEDPFGEEFGICKDCPYGTFGMDCLETCNCQSGICDRGTGKCLKFPFFQYSVTKSSNR-FVSL 149
Rat_ESM1 TERDAASGDGNAVREEICDRNAARPSVM-KWLNPR 184
Mouse_ESM1 TERDSASGDGNAVREEICEGNAARPSVM-KWLNPR 184
Human_ESM1 TEHDMASGDGNIVREEQVKENAAGSPVMRKWLNPR 184
SEQ ID NO:5
SEQ ID NO:6
SEQ ID NO:2

FIGURE 4



Exon	ESM-1		
	acceptor site	donor site	exon size
1	CAGCT	CAAAGgtaaa	378
2	cccagACTGT	CACGGgtaag	150
3	ttcagAGCAT	GATAC	1568

FIGURE 5

ESM-1 Fold Change of Expression in Various Tumors by Microarray Analysis

Tumor[a]	Patient 1	Patient 2	Patient 3	Patient 4	Patient 5	Patient 6	Patient 7	Patient 8	Patient 9	Patient 10	Patient 11	AVE
Breast	-1.20	-1.18	1.37	1.36	1.14	-1.09	-1.05	1.77	1.07	1.86		0.41
Colon	1.71	2.07	1.60	2.51	1.39	-1.05	1.82	1.08	2.27	1.51		1.49
Kidney	1.62	2.07	2.23	1.34	2.84	1.61	1.80	1.85	1.38	1.06		1.78
Lung	1.98	1.26	1.14	3.07	3.21	2.28	2.56	4.01	3.57	2.98	3.39	2.68

[a] Each tumor type represents a different set of patients.

FIGURE 6

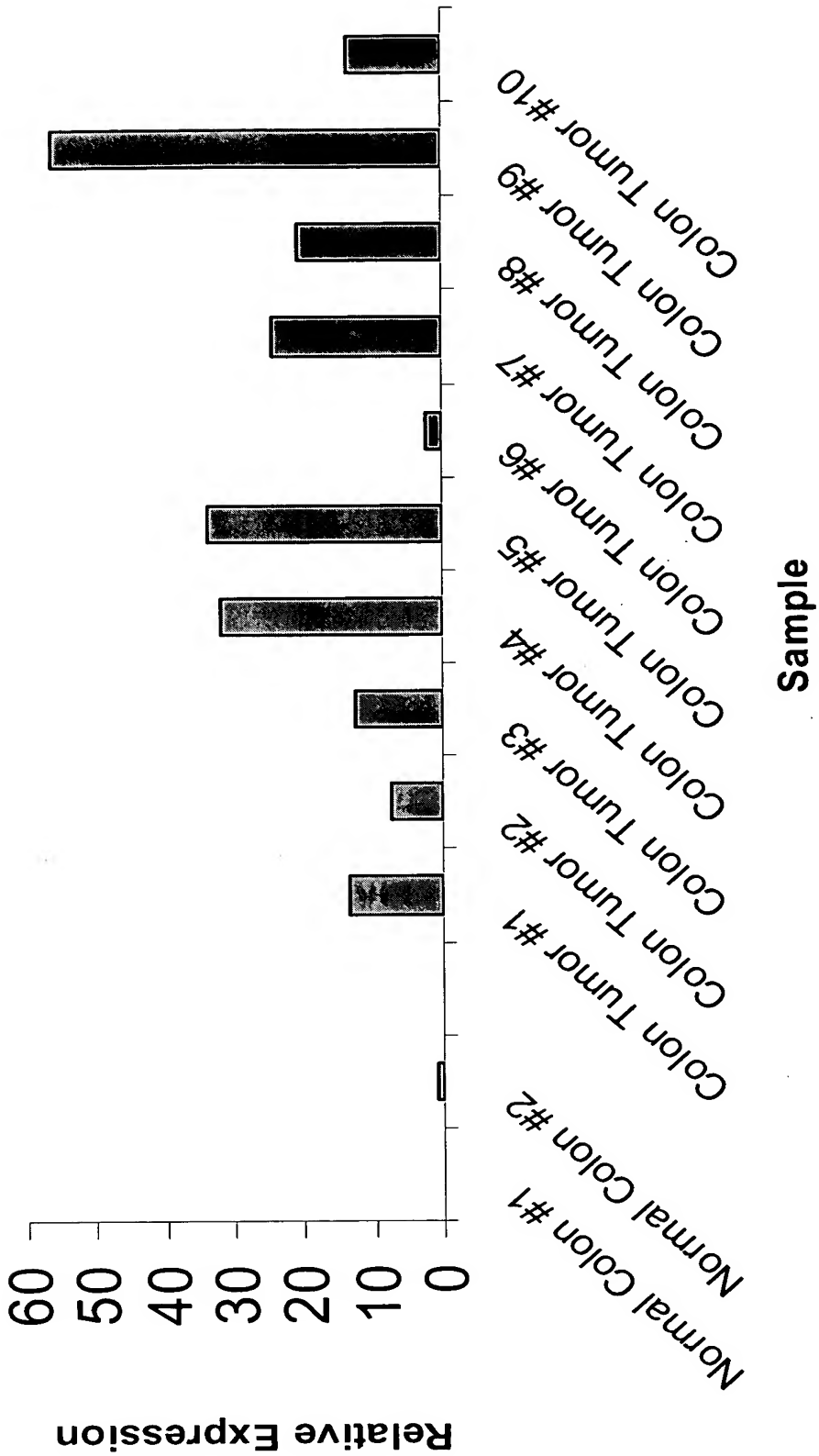

Relative Expression
60
50
40
30
20
10
0
Normal Colon #1
Normal Colon #2
Colon Tumor #1
Colon Tumor #2
Colon Tumor #3
Colon Tumor #4
Colon Tumor #5
Colon Tumor #6
Colon Tumor #7
Colon Tumor #8
Colon Tumor #9
Colon Tumor #10
Sample

FIGURE 7

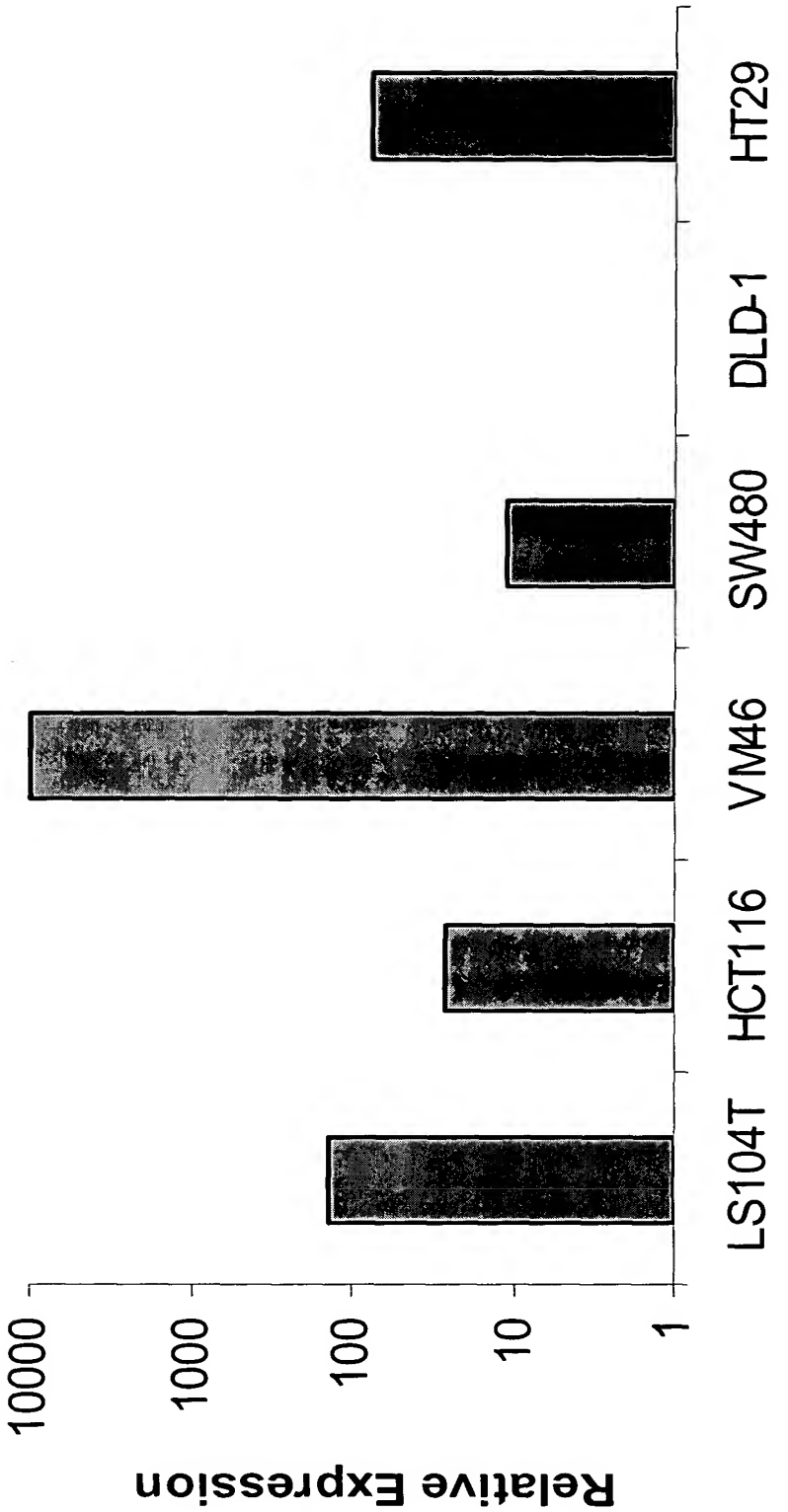

Relative Expression
10000
1000
100
10
1
LS104T
HCT116
VM46
SW480
DLD-1
HT29
Cell Lines

FIGURE 8

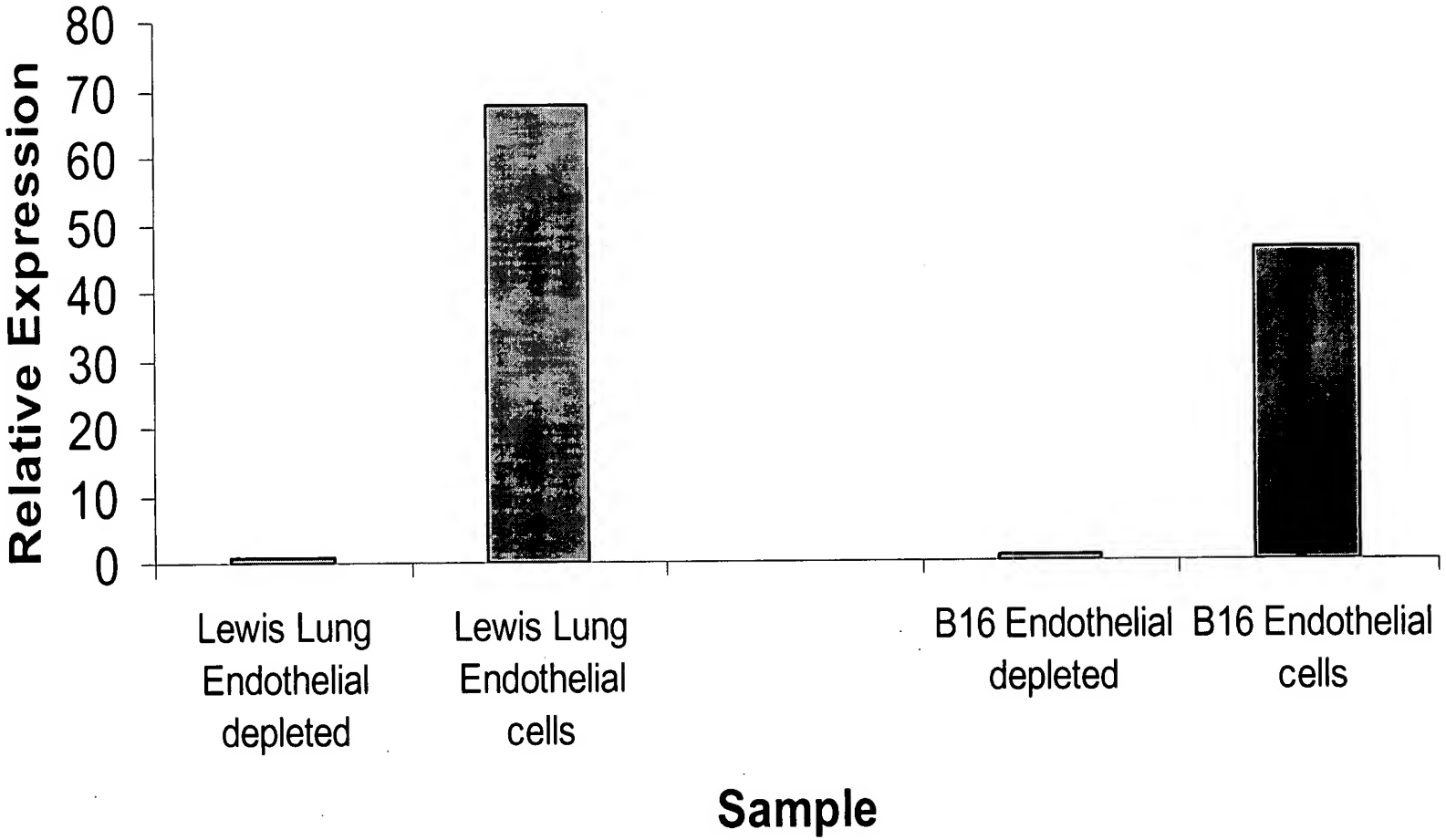
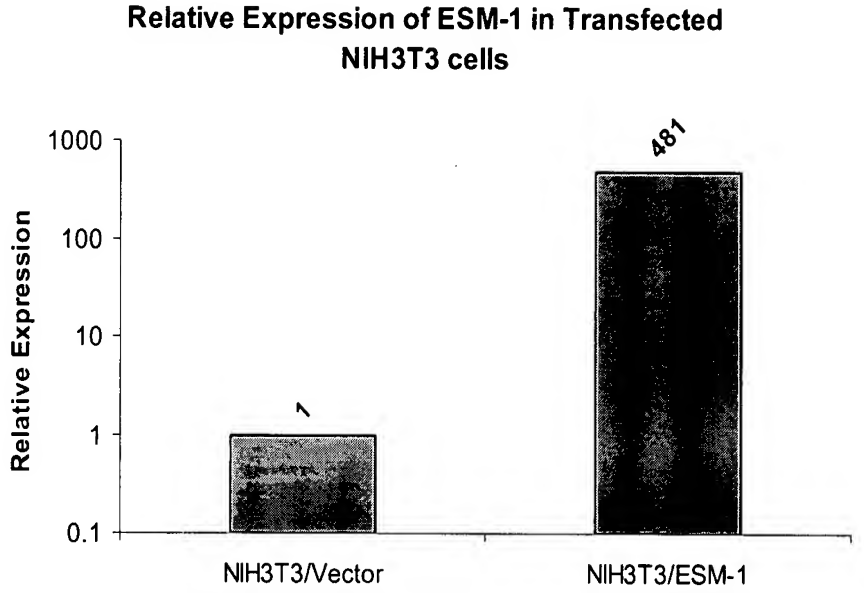

Relative Expression
80
70
60
50
40
30
20
10
0
Lewis Lung Endothelial depleted
Lewis Lung Endothelial cells
B16 Endothelial depleted
B16 Endothelial cells
Sample

FIGURE 9

A


Relative Expression of ESM-1 in Transfected NIH3T3 cells
Relative Expression
1000
100
10
1
0.1
1
481
NIH3T3/Vector
NIH3T3/ESM-1

B

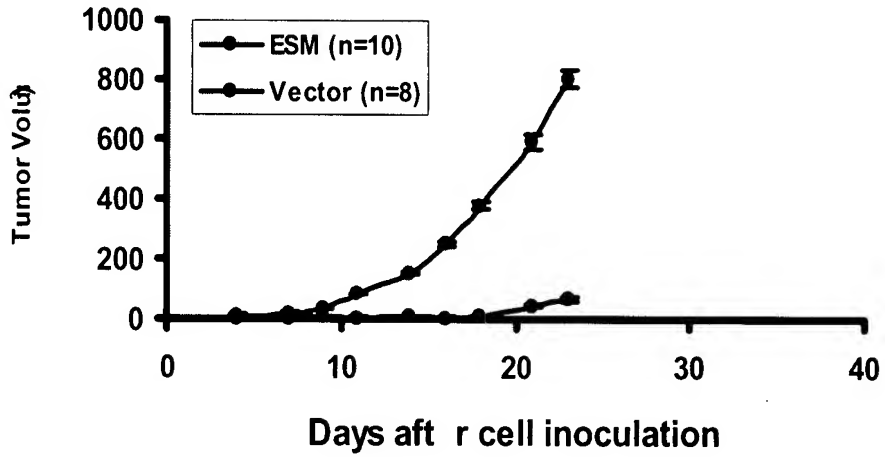
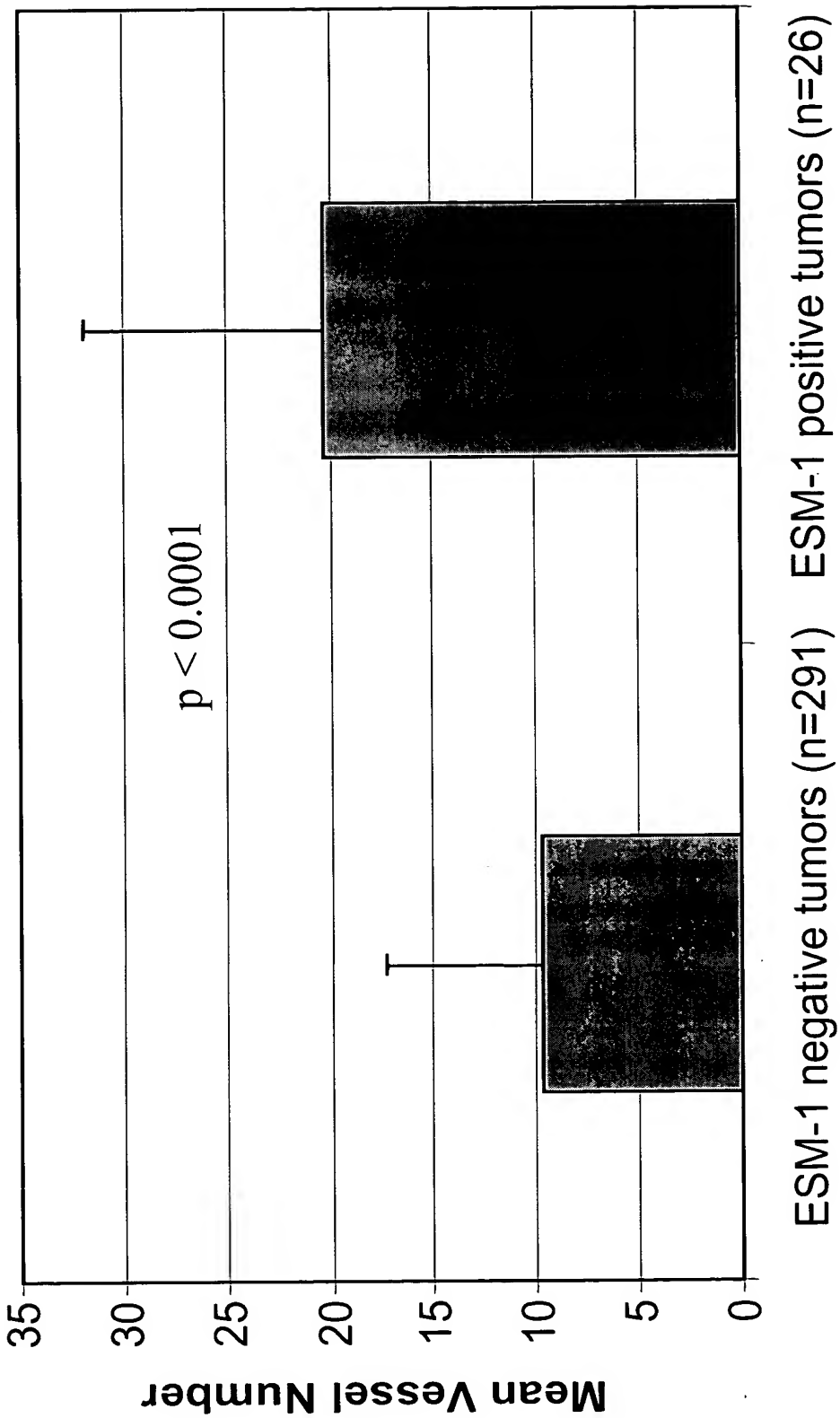

NIH3T3/ESM Kinetics
Tumor Volu
1000
800
600
400
200
0
ESM (n=10)
Vector (n=8)
0
10
20
30
40
Days aft r cell inoculation

FIGURE 10

ESM-1 expression
number of samples (percentage)

tumor	breast	5 (9.6)
	colon	0 (0.0)
	kidney	16 (28.1)
	lung	4 (7.7)
	ovary	0 (0.0)
	prostate	1 (2.1)
normal	breast	0 (0.0)
	colon	0 (0.0)
	kidney	1 (6.3)
	lung	0 (0.0)
	ovary	1 (7.1)
	prostate	0 (0.0)

FIGURE 11


Mean Vessel Number
35
30
25
20
15
10
5
0
p < 0.0001
ESM-1 negative tumors (n=291)
ESM-1 positive tumors (n=26)